From:

Leffers, Gerald

Sent:

Tuesday, January 25, 2005 4:06 PM

To:

STIC-Biotech/ChemLib

Subject:

FW:10/776,213 sequence search

Examiner's mailbox is in 2c70 of Remsen. Thank you. Gerry Leffers

Gerald G. Leffers Vr., PhD Primary Examiner, Art Unit 1636 Remsen Building, Room 02A69 (571) 272-0772

-----Original Message-----

From:

Leffers, Gerald

Sent:

Tuesday, January 25, 2005 4:02 PM

To:

STIC-Biotech/ChemLib

Subject:

09/776,213 sequence search

Please do a search/interference search for SEQ ID NO: 2 of this application (~723 nucleotides). Claims are to sequences comprising as few as 17 consecutive nucleotides of SEQ ID NO: 2. Thank you. Gerry Leffers

Gerald G. Leffers Tr., PhD Primary Examiner, Art Unit 1636 Remsen Building, Room 02A69 (571) 272-0772

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Unclassified.
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1 (bases 1 to 723)
Belfield,G.P. and Oakley,C.
Compositions and methods utilizing the yeast ZE01 promoter Compositions and of APR-2004;
Patent: US 6716601-A 2 06-APR-2004;
Location/Qualifiers
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Sequence 24
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Belfield,G.P. and Oakley,C.
Belfield,G.P. and Oakley,C.
Compositions and methods utilizing the yeast ZEO1 promoter
Patent: US 6716601-A 24 06-APR-2004;
Location/Qualifiers
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     CTCCCCGCACGATTTCTTCCTTCATATCTTCCTTTATTCCTATCCCGTTGAAGCAACC
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Sequence 20
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Belfield,G.P. and Oakley,C.
Compositions and methods utilizing the yeast
Patent: US 6716601-A 20 06-APR-2004;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                Unknown.
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                                                    ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGGAT
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                                                                                                                                                                                                                                                                                                                                                  SC9920 23498 bp DNA S.cerestisiae chromosome XIII cosmid 9920. 248639 Z71257 248639.1 G1:732924 COX7; cytochrome oxidase; delta element; PETIII; transfer RNA-Ala.
                    All CDS over 100 codons have been analysed. CDS that are completely overlapped and those that are overlapped by more than 50% of their length by a larger CDS have been omitted from this
                                                            Notes:
All CD
                                                                                                 Direct Submission
Submitted (10-MAR-1995) Saccharomyces cerevisiae chromosome XIII
sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge
CB10 1RQ E-mail: barrell@sanger.ac.uk
                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae Saccharomyces cerevisiae
                                                                                                                                                                          2 (bases 1 to 23498)
Barrell,B., Rajandream,M.A. and Walsh,S.V.
                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 23498)

Hunt,S. and Bowman,S.
                                                                                                                                                                                                              Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCCGGAGAACATAGTGATAAGGGATGTAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCCTATTTGGGTAAGCCCCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCTTCCTATTTGGGTAAGCCCCCTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is given for each CDS.
Cosmid 9920 is overlapped at the start of this sequence by cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAA88574.1"
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KUPAKINALMAVFQEQLLMLVKEIVVNERBEDISERYSKESSERFYHRHISAVLL
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KUPAKINAKLAYKLLKSLTHITSKNILKVCFVLBSLIMLLATLDDLYEDGTIWSYDKS
FSARNSAEVLNEFWTNFLKFAEDSSERFXKHVSFLDVYLEWLFFWQSTVGNYS
FSARNSAEVLNEFWTNFLKFAEDSSERFXKHVESEIFNSLSCCKSLSEYTKLNQTLS
FSARNSAEVLNEFWTNFLKFAEDSSERFXKHVESEIFNSLSCCKSLSEYTKLNQTLS
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LYIEDPKNYKFNDSGEIFKGNNKFLNGRTITTLYRSAVANGQUEGFCAVLSKLDETF
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LYYDFGHTFERGKVNLNFSDIVGNYLQPANGGDAMLTFDIAESNUSVFFYYSRVLY
GAKEKYVTHAVELINGCNDTSQIFFPANAIEVFARYWFAIDTKSELVSSLSTNTHLL
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COMPLIEMENT (2406. .2438)
/note="PS00061 Short-chain alcohol dehydrogenase family
signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at the end of this sequence Location/Qualifiers
                                                                                                                  complement (4197.
                                                           note="possible splice acceptor sequence,
                                                                                                                                                                 ALAHLCAIYTE"
                                                                                                                                                                                                                 /product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                   small spliced gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (join (4101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(4101. .4196
/note="YM9920.02c, unknown,
small spliced gene"
/coden state
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="YM9920.03c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="tRNA-Ala, anticodon agc, len: 73"
complement (3379. .3706)
/note="delta element"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="tRNA-Ala"
'note="tRNA->1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (3200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complement (<1. .2870)
/note="YM9920.01c, unknown, ps00061 Short-chain alcohol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4932"
/chromosome="XIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Saccharomyces
/mol_type="genomic DNA"
/strain="AB972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .23498
                                                                                                                  .4199)
                                                                                                                                                                                                                                                                                                                                                                                                           .4196,4434. .4505))
known, len: 55, CAI: 0.13, possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4196,4691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by cosmid 8156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          len: 61,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4780))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAI: 0.17, possible
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LLIVDIESILTKLHSYEKVCHHIELASEQTPERKSSFIYEMLLALASPQDDIPTPDE
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/note="possible splice branch sequence, tacomplement (428. .4433)
/note="possible donor squence, gtatgt"
complement (4685 . .4690)
/note="possible donor squence, gtcagt"
complement (4689 . .4694)
/note="possible donor squence, gtcagt"
5632 . .7389
/note="YM9920.04, unknown, len: 585, CAI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFKNEQLGTNNDNMKSGSRFSHPSFKQLLIQK"
complement(10777. .12021)
FSLITAIVSFIGINTIPSMKFQIPHSKKQWILFGNLGVSGFIFQLLLTMGIQRERAG
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complement (10146 . 10550)
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/note="YM9920.05, unknown, len: 366, CAI: 0.11, s
YK56 YEAST P36156, YKR076W, hypothetical protein
62.6% identity in 369 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="YM9920.06c, unknown,
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22-NOV-2002

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Query Match
Best Local Similarity
Matches 721; Conserv
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TTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTCAA
                                                                            TGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACATAGTGATAAGGGATGTAAC
                                                                                                                           GTCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCCGCCGCCGTTTCCCCA
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complement(12446..12754)
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questionable orf"
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AX536716
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Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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Bax-responsive
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TGGGACGTCTTAACTTTTATTGCAGAGGACTATCAAATCATACAGATATTGTCAAAAAAA
                                                                                                                             GTGATAAGGGATGTAACTTTCGATGAGAGTTAGCAAGCGGAAAAAAACTATGGCTAGC
                                                                                                                                                                                           TTGGGTAAGCCCCTTTCTGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACATA
                                                                                                                                                                                                                                                     GCGGCGCCCGTTTCCCAATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCCTAT
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                                                            TGGGAGTTGTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTC
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PHARMACEUTICA N.V. (BE)
Location/Qualifiers
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Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases I to 257757)
Gardner,M.J., Hall,N., Funo R Marin
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Plasmodium falciparum 3D7 chromosome
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Dorner, F., Scheiflinger, F. and Falkner, F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
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166494
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     Hyman, R.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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/locus tag="PP11 0071"
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/locus tag="PP11 0071"
complement (2647...4074)
/locus_tag="PP11 0071"
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/product="Ruvb DNA helicase, putative"
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DEKYSMFFDNSCGLVGQFKAREASLFLVDLIKQKKLAGKCILLAGPSGSGKSALAIGI
SREINKMPFVFLSGGEVYSNEIKKTEVILEAFRKSIHIKIKEEKLVYEGEVVDMVVE
ENECLYSLNGAKQINAIIITLKSVKGSKTLRADFKHHEQIAREKIKIGDTY1ETNTG
HVKRLGRCNDYAKEYDINAIITLKSVKGSKTLRADFKHHEQIAREKIKIGDTY1ETNTG
HVKRLGRCNDYAKEYDINAIITLKSVKGSKTLRADFTUGELHDIDLAHMIDIECFSY
LNRALESFLAPILTMATNRGICTVKGTDNIEEPHGIPVDLLDRLIIKTFPYTLKEIVQ
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2199. .2240
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VVPRIYGKHLFVEKRQFPSTLYFVTTILMMRDVTKIHAVLVAYERRKSLEFFVLGIKK
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/protein_id="AAN35659.1"
/db_xref="GI:23495997"
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/mol_type="genomic DNA"
/isolate="3D7"
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 complete sequence.
BX663508
BX663508.8 GI:40714027
HTG.
                                                                      BX663508 170295 bp DNA linear VRT 06-JAN-2004 Zebrafish DNA sequence from clone CH211-144B6 in linkage group 22,
                                                                                                                                                                                                              AATCATACAGATATTGTCAAAAAAAAAAAAAAGACTAATAATAACA 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with rished as mall overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeates; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession the WORMPEP database can be found at hitp://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the this is found the longest good quality representation will be submitted.
                                                                                                                                                                                                                                                                                                   78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-144B6 is from a CHORI-211 BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-JAN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jan 6, 2004 this sequence version replaced gi:37805672.
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Contact: zfish-help@sanger.ac.uk
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Submitted (19-SEP-2001) Genome
University School of Medicine,
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Homo sapiens BAC clone RP11-107
AC092573 AC015764
AC092573.2 GI:15668084
                                                                                                                    Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Sep 19, 2001 this sequence version replaced gi:14916158.
                                                                                                                                                                                                          MO 63108, USA 5 (bases 1 to 171265) Waterston, R.
                                                                                                                                                                                                                                                                                                                     4 (bases 1 to 171265) Waterston, R.H.
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Submitted (19-UUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
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The sequence of Homo sapiens BAC clone RP11-107 Unpublished (2001)
3 (bases 1 to 171265)
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Tomlinson, C., Cotton, M
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Mammalia; Eutheria; Primates;
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Sulston,J.E. and Waterston,R.
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           Center project name: H_NH0001007
                                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
Drafting Center: WIBR
                                                  Contact: sapiens@watson.wustl.edu
                                                                  Web site: http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elliott,G.,
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                                                                                                                                                                                                                                                                Sequencing Center, Washington 4444 Forest Park Parkway, St.
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                                                                                                                                                                                                                                                                                                                                                                       Louis,
                                                                                                                                                                                                                                                                   Louis,
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between neighboring data submissions. clone sections once, This sequence may not represent the entire insert of this It may be shorter because we only sequence overlapping ections once, or longer because we provide a small overlap

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E Frengen, E.,

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FEATURES
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The clone sequenced to the left is RP11-291G2, 1984 bp overlap; the clone sequenced to the right is RP11-158LB. Actual start of this clone is at base position 105122 of RP11-291G2; actual end is at base position 171265 of RP11-107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8 The clone may be obtained either Research Genetics, Inc. (http://www.resgen.com) or Pieter de and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of AC015764 has been incorporated into AC092573.
Location/Qualifiers
1. .171265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphisms have been identified between AC013461, AC015764 and {\tt AC012052}.
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                                                                                                                                      note="match to EST
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
                                                       'note="match to EST
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7. .3996
te="match to EST AL537636
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                      .y="L2"
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                                                             BE867724
                                                                                               (NID:g7907664)"
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Matches 102;
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GCTATAAAAAGGAGAAATTAATCCACACAATCTCACACATTCTGGGAGGAAAAATAAACT
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/note="similar to Homo sapiens
(NID:g10153317)"
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/note="similar to
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'note="match to EST W25250 (NID:gl303104) zb68e09.rl"
| 787. .9076
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         Contact: sequence submissions@genome.wi.mit.edu

Contact: sequence submissions@genome.wi.mit.edu

Contact: sequence submissions@genome.wi.mit.edu

Center project name: L1385

Center clone name: 337 F 19

Center clone name: 337 F 19

Center clone name: 337 F 19

Chemistry: Dye-primer-amersham; 3% of reads

Chemistry: Dye-primer-amersham; 3% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 19930 bases at least Q40

Consensus quality: 19935 bases at least Q40

Consensus quality: 203385 bases at least Q40

Consensus quality: 203385 bases at least Q40

Consensus quality: 203385 bases at least Q20

Insert size: 206529; sum-of-contigs

Quality coverage: 4.0 in Q20 base:

NOTE: This is a 'working draft' sequence. It currently

* consists of 23 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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1 (bases 1 to 208729)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-OCT 1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 21, 2000 this sequence version replaced gi:7321517. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Homo sapiens chromosome 2, clone RP11-337F19
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
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64715 contig of 8064 bp in length
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Carvelli, K., Chacko, J., Chen, J., Di, W., Ding, Y., Dugan, S.,
Durbin, J., Forcum, J., Ganesh, R., Garcia, C., Goodman, M.,
Gorrell, J.H., Haywood, M., Hernandez, J., Jackson, L., Jin, S.,
Kampal, R., Karpathy, S., Kovar, C., Leal, B., Li, Y., Lichtarge, O.,
Liu, W., Logan, O., Lu, J., Ly, T., Martinez, C., Oswal, G., Perez, L.,
Rashid, N.D., Rowland, K., Savage, L., Scherer, S.E., Shen, H.,
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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On Aug 25, 1998 this sequence version replaced gi:3402643.
Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality does not meet this standard, it will be indicated in the annotation.
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of Molecular and Human Genetics, Baylor College of Medicine,
Baylor Plaza, Houston, TX 77030, USA
6 (Dases 1 to 80659)
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Direct Submission
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Baylor Plaza, Houston,
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The repeat regions shown were identified using RepeatMasker by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 80659)
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                          /rpt_family="MER53"
4687. .4829
                                                                                                                                                                            complement (1641.
                                                                                                      complement (3587.
                                                                                                                      , rpc
                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="X"
                                                                                                                                                                                                                                                                           function="clone overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (11-APR-1998) Molecular and Human Genetics, Baylor
E Medicine, One Baylor Plaza, Houston, TX 77030, US
      rpt_family="MER58"
                                                                                                                                                                                                                                                                                             note="overlaps bases 114570.
                                                                                                                                                                                                                                                                                                                                   lone="GSHB-223P11"
                                                                                                                                                                                                                                                                                                                                                                                                                                    .80659
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                                                                                _family="MIR"
                                                                                                                                                        family="Aluy"
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                                                                                                                                                                                                   family="MIR"
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                                                                                                    .3670)
                                                                                                                                                                              .1930)
                                                                                                                                                                                                                                                                                                 .116568 of clone AC112492"
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repeat_region

repeat_region repeat_region

complement (5319. .5358)
/rpt_family="AT_rich"
complement (5853. .5898)
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complement (5943. .6244) /rpt_family="MLT1E" complement (6228.

repeat_region repeat_region

complement(6631..6758)
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complement(7635..7690)

_family="(CA)n"

_family="MER3"

complement (6354. .6624)
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family="MLT1D" ement(635/

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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33326 GAACATAGTTGTCAAGAGTTCAAACTCCGAGTTCAAAGTTAGCATGTTTTTAGAAAATAA 33267
                                                                                                                                                                                                                                                                                                                      697 AAAAAAAAAAAAGACTAA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 GAACATAGTGATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTAT 576
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 195932)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome X, clone RP11-12D5
                                                                                                                                                      195932 bp DNA linear HTG 04-APR-2000 Homo sapiens chromosome X clone RP11-12D5 map X, WORKING DRAFT SEQUENCE, 9 unordered pieces.
                                                                                  AC021710.4 GI:7408016
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                          ATGAAAAAAAAAAAAAA 33129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCTAGCTGGGAGTTGTTTTTCAATCATATAAAAAGGGAGAAATTGTTGCTCACTATGTGA 636
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ilarity 51.0%;
Conservative
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/rpt_family="AT_rich"
complement(35418. .35439)
/rpt_family="AT_rich"
complement(38090. .38123)
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complement(32126. .32237)
/rpt_family=""/"
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32378. .32676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /standard_name="DXS67"
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/rpt_family="(TAA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (28196. .28279)
/rpt_family="L2"
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complement(26295...2)
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25357. .26294
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db_xref="dbSTS:32826"
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3. .26927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42.8; DB 9;
Pred. No. 0.52;
0; Mismatches 97;
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complement (13783.

family="L1PA8"
. . . 14150) family="MIR"

complement (16745. .17110) /rpt_family="L1M4"

_tamily="L2"

family="MLT1C"

complement (10630...10701)
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complement (11161...11220)
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complement (9246. .9302)
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complement (9663. .10244

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ement(10630

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complement (12725. .12846)
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complement (12853. .12932)

family="(CATA)n"

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21094

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20350. .20551

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complement(18177. ...

family="LIMA9"

7. 19856

repeat_region repeat_region

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25211. .25359

/rpt_family="AluSp"
complement(22905..22958)
/rpt_family="MIR"

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 4, 2000 this sequence version replaced gi:6939568. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 189137 bases at least Q40
Consensus quality: 192288 bases at least Q30
Consensus quality: 193686 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 195132; sum-of-contigs
Quality coverage: 5.0 in Q20 bases; sum-of-contigs
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                          49151
49251
73383
73483
104625
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Center clone name: 12_D_5
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                      ocation/Qualifiers
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104624: contig
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1379: gap of 100 bp
0400: contig of 9021 bp in length
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14: contig of 8994 bp in length
4: gap of 100 bp
15: Cartillo of 1300'
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93: contig
93: gap of
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                                                                              AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            517 GAACATAGTGATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTAT 576
Submitted (08-MAR-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Mar 12, 2001 this sequence version replaced gi:13092292.
During sequence assembly data is compared from overlapping clon where differences are found these are annotated as variations
                                                                                                                                                                                                                                            complete sequence.
AL359542
                                                                                                                                                                                                                                                                            Human DNA sequence from clone
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                              Homo sapiens
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                                                                                                 Direct Submission
                                                                                                                Heath, P
                                                                                                                                                                                             Homo sapiens (human)
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142494. .195932
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104725. .142393
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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e RP6-190D15
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me XQ25-26.1,
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.216 of consensus"

FEATURES source repeat_region together with a note of the overlapping clone name. Note that the variation amnotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the IMPORTANT: This sequence is not the entire insert of clone RP6-190D15 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP4-537K23 is at 28759 in this sequence. The true right end of clone RP4-753P9 is at 100 in this sequence. Location/Qualifiers http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X constructed by the Sanger Centre Chromosome X mapping Group. Further information can be found at SWISSPROT; ${\tt Tr:}$, ${\tt TREMBL}$; ${\tt Wp:}$, ${\tt WORMPEP}$; ${\tt Information}$ on the WORMPEP database can be found at assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers in the feature table with their source databases: Em:, EMBL; 5914. .6224 /note="AluYb8 repeat: matches 1. .311 of consensus" 11889. .12080 /note="AluSg repeat: /note="liMB3 repeat: matches 6035. .6127 of consensus" 10464. .10518 /note="75K repeat: matches 1. .53 of consensus" 10835. .11133 3076. .3129 /note="27 copies 2 mer tc 77% conserved" #818. .9104 |mote="AluSg1 repeat: matches 1. .289 of consensus" 3758. .8796 note="L1MB8 repeat: matches 6133. 'map="q25-26.1" 'clone="RP6-190D15" /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606" note="AluSg repeat: matches 253. .294 of note="38 copies 2 mer aa 69% conserved" .0287. .10362 note="I note="AluSx repeat: matches 1. note="AluY repeat: matches 1. .300 of consensus" clone_lib="RPCI-6" note="24 copies 2 mer note="AluSx repeat: matches 1. note="AluSx repeat: matches 5. note="AluSq repeat: matches 1. chromosome="X" .28858 7. .8469 e="L2 repeat: matches 2602. .2728 of . 646 IMB8 repeat: matches 4267. .6133 of consensus" matches gt 72% conserved" 24. .298 of consensus" .302 of consensus" .312 of consensus" .299 of consensus" .296 of consensus" .6171 of consensus" in this sequence. consensus" given 얁

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               /note="AluSc repeat: matches 1. .306 of consensus" 27397. .27415
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13957. .14317
/note="LIM4 repeat: matches 4795.
                                                                                                                                                                                                                                                                          /note="AluSx repeat: matches 1. .216 of
23986. .24027
                                                                                                                                                                                                                                                                                                                                                                                        23037. .23338
                                                                    note="MER51B
                                                                                                                                                                                                                                        'note="Alu repeat: matches 259. .298 of consensus"
24570. .24787
                                                                                                          'note="AluSx repeat:
                                                                                                                                                                                                                   note="L1ME repeat:
                                                                                                                                                                                                                                                                                                                                                                 note="AluSx repeat: matches 1. .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                  note="MIR repeat: matches 115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="AluY
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6081..16168
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                                                                                                                                            note="49 copies 2 mer ag 61% conserved"
                                                                                                                                                                              note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                                                                                                                                                                                             note="L1M4 repeat: matches 5627. .5818 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                        note="U6 repeat: matches 1. .30 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           391. .20689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="L1PA12 repeat: matches 5937. .6158 of consensus" 9745. .20039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Weakly double-stranded"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="AluSq repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5171. .15249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1MB4 repeat: matches 5646. .6176 of consensus"
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repeat: matches 525. .543 of consensus"
                                                                      repeat: matches 453. .526 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              matches 5489. .6163 of consensus"
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                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SMISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 29, 2002 this sequence version replaced gi:21727348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.
                                                    constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.
                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-246F18 is from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Wellcome Trust Sanger Institute Center code: SC
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                                                                                                                                                                                                        database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note="L2 repeat: matches 2535. .2736 of consensus"
28662. .28805
/note="MIR repeat: matches 110. .256 of consensus"
                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.sanger.ac.uk
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No.	Score	Match	Match Length	BG	ID	Description
ב	723	100.0	723	4.	AAD07475	Aad07475 Yeast pro
N	723	100.0	11427	4	AAD07497	pYMR25
w	723	100.0	13073	4.	AAD07493	-
4	720.4	99.6	850	4	AAD07503	Aad07503 Yeast YMR
ហ	497.4	68.8	680	σ	ABQ76446	
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8	38.4	5.3	544	11	ADT96256	Adt96256 Colon can
9	37.8	5.2	7736	տ	AAS29224	Aas29224 Genomic s
10	37.8	5.2	7736	տ	ABA16123	Aba16123 Human ner
11	37.8	5.2	7736	σ	ABS68364	Abs68364 Human DNA
12	37.8	5.2	7736	10	ADC25486	Adc25486 Human cDN
13	37.4	5.2	386	ហ	ABV04394	Abv04394 Human pro
14	37	5.1	366	4	AAL35477	Aal35477 Human mus
15	37	5.1	366	œ	ABX58465	Abx58465 cDNA enco
16	37	5.1	366	12	ADJ28192	Adj28192 Human mus
17	37	5.1	390	8	ABX36811	Abx36811 Bovine ES
18	37	5.1	400	0	ABQ59188	Abq59188 Human col
19	36.4	5.0	201	13	ADS41207	Ads41207 Human aut
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ADQ97316	ADS89390	ACN88712	ADA71938	AAZ41383	ABV96856	ACA64924	AAK70003	ABV18166	ACN37231	ADI82483	ADH29006	ABK09744	ABL58962	ACH17729	ADS89438	ACA40062	ADA56114	ACC50510	ADA39926	AAZ00806	ACN62578	ABL34113	ABT22885	ADS36499
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ALIGNMENTS

RESULT 1
AADO7475
ID AADO7475
ID Yeas
AC AADO
AC AADO
AC Yeas
KW Yeas
KW nonXX
Sacc
PN WO20
PN WO20 17-NOV-2000; 2000WO-SE002277. 31-MAY-2001 Yeast promoter YMR251WA. AAD07475; AAD07475 standard; DNA; 723 BP. 23-NOV-1999; WO200138549-A1 Saccharomyces cerevisiae. Yeast; promoter; gene expression; fermentable carbon source; glucose; non-fermentable carbon source; ethanol; yeast cell culture; ds. 10-AUG-2001 (first entry) (ASTR) ASTRAZENECA AB. 99SE-00004247.

New promoter sequences from Saccharomyces cerevisiae useful for controlling expression of homologous and heterologous nucleic acid expression in yeast cells.

WPI; 2001-367697/38.

Belfield G,

Oakley

Claim 1; Page 67-68; 191pp; English.

The invention relates to yeast promoters that are used to control the expression of homologous and heterologous nucleic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as glucose or a non-fermentable carbon source such as ethanol or both. Therefore expression of nucleic acid molecules encoding a polypeptide under the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters

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RESULT 2
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AC AADO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are useful for, inter alia, the high level production of proteins on polypeptides in yeast cell culture. The present DNA sequence is saccharomyces cerevisiae YMR251WA promoter related to the invention
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         plasmid
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New promoter sequences from Saccharomyces cerevisiae useful for controlling expression of homologous and heterologous nucleic ac expression in yeast cells.
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                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae Unidentified.
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The invention relates to yeast promoters that are used to control the expression of homologous and heterologous nucleic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as ethanol or both. Therefore expression of nucleic acid molecules encoding a polypeptide unto the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters are useful for, inter alia, the high level production of proteins or polypeptides in yeast cell culture. The present sequence is pYMR251AP plasmid related to the invention. This plasmid contains pPRB1 and yeast YMR251MA promoter Example 4; Page 133-143; 191pp; English

Sequence 11427 BP; 3131 A; 2589 C; 2527 G; 3180 T; 0 U; 0 Other;

Length 11427;

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The invention relates to yeast promoters that are used to control the expression of homologous and heterologous nucleic acids encoding proteins and polypeptides in yeast cells. The yeast promoters are induced by a fermentable carbon source such as glucose or a non-fermentable carbon source such as ethanol or both. Therefore expression of nucleic acid molecules encoding a polypeptide under the control of the novel yeast promoters are regulated by varying the level of a fermentable carbon source or a non-fermentable carbon source or both. The yeast promoters
                                                                                                                                                        New promoter sequences from Saccharomyces controlling expression of homologous and rexpression in yeast cells.
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                                                                                                                               Example 3; Page 88-99; 191pp; English.
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RESULT 4
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100.0%; Pred. No. 3.5e-210;
ative 0; Mismatches 0;
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Yeast YMR251WA promoter region.

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Query Match
Best Local Similarity
Matches 721; Conserv
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                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New promoter sequences from Saccharomyces cerevisiae useful for controlling expression of homologous and heterologous nucleic a
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                                                                 ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGGAT
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                                                                                                                          TCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTT
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                                                                                                                                                                                      TTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAA
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닭 8 밁 Ś В Ś 밁

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ABQ76446 standard; cDNA; 680 ВP

21-NOV-2002 (first entry)

S. cerevisiae BAX-associated cDNA fragment SEQ ID 317.

RESULT 5
ABQ76446
ID 76446
ID 76446
ID 76446
AC ABQ7
XX ABQ7
XX Bax;
KW Bax;
KW Vaso
KW Papop
KW apop
XW apop
XW meux
XX Sacc
XX WO20
XX WO20
XX Sacc
XX Sacc
XX WO21
PD 22-A
XX O3-D
PF 21-D
PR 04-J
PR 04-J vasotropic; vaccine; gene therapy; proliferative disorder; cancer; apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia; neurodegeneration; cell death; ss. Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide; vasotropic; vaccine; gene therapy; proliferative disorder; cancer;

Saccharomyces cerevisiae

WO200264766-A2

22-AUG-2002.

21-DEC-2001; 2001WO-EP015398.

22-DEC-2000; 04-JAN-2001; 09-JAN-2001; 2000EP-00870318. 2001EP-00870002. 2001EP-00870003.

(JANC) JANSSEN PHARM NV

á 밁 Ś DP. δ

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This invention describes a novel nucleic acid representing a synthetic Eax gene. The Bax gene of the invention is useful for identifying Bax-CC resistant yeast or fungi, identifying, or obtaining and identifying CC Candida spp. sequences that are differentially expressed in a pathway CC eventually leading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax-induced cell death. The products of the CC invention have cytostatic, fungicide; immunosuppressive, virucide and CC vasotropic activity and can be used in vaccines or for gene therapy. The CC isolated nucleic acids, polypeptides, pharmaceutical compositions, CC antisense molecules and antibodies are useful as medicaments or in CC preparing a medicament for treating, preventing and/or alleviating CC diseases associated with yeast or fungi or proliferative disorders, such as cancer, or for preventing apoptosis in certain diseases. The compounds CC or polypeptides, or the genetically modified organism are useful for CC preparing a medicament for modifying the endogenic flora of humans and cother mammals. The vaccine is useful for immunising against yeast or fungal infections. Apoptosis-related diseases include autoimmune disease, CC ischaemia, diseases related with viral infections or neurodegenerations. CC This sequence represents a polymucleotide associated with the Bax gene CC described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 498;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB;
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                                                                                                                                               TGGGACGTCTTAACTTTATTGCAGAGGACTATCAAATCATACAGATATTGTCAAAAAAA
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Pred. No. 1.3
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2000 BP; 336 A; 265 C; 284 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method (M1) for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                  CATTCACTTTCTTTTCCCTTCGCGGTCCGGACCCCGGGACCCCTCCTCTCCCCGCACGATT
                                                                                                                                                                                                                                                                                                                                       AKYKSGSMSKRMWMSSCGRSGCGRRSAYSRYYGTSRKYGTYKKMTYYSASRCMRAYMTTS
                                                                                                                                                                                                                                                                                                                                                                                                AGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGGATGGGGGCTAAGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W, Co
F, Quan S,
WRMWRMTRRRWAKKSSRTSRRKKRKWCMRKRKYKRMRGYSRMRSCKRARWMKRCRSGRA
                                                        TGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTATCTCACAGTGGTAACGGCACCGT 314
                                                                                                                                                                                                                         YSWACSSYTWCRSKRRSMMWKMMRKMRWSRSYGWYSWSYKMWMCTAYKKSYYSRWCYMYR 303
                                                                                                                 GGGWRGATRYWGRGYMSRMAMMYKKMYWYRGYKGMKRGWWAGRMMMRSMCRWSKACYYMR
                                                                                                                                                                TCTTCCTTTCATATCTTCCTTTATTCCTATCCCGTTGAAGCAACCGCACTATGACTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 5263; 899pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
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S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA; 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.1%;
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58; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 8; Pred. No. 0.66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
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Whitham S, Xie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 T; 0 U; 752 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goff SA,
ie Z, Zhu
                                                                                                                                                                                                                                                                                                                                                                                                                                                        248;
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on. M1
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                                                                                                                 363
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RESULT 7
ABS51325/c
ID ABS51325/c
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ID ABS51325/c
ID ABS51325/c
ABS51326/c
ABS5126/c
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                                17-JAN-2001;
19-JAN-2001;
19-JAN-2001;
19-JAN-2001;
19-JAN-2001;
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19-JAN-2001;
19-JAN-2001;
19-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secretory polypeptide; SPTM; actinic keratosis; arteriosclerosis; bursitis; cirrhosis; hepatitis; polycythaemia vera; anaemia; psoriasis; primary thrombocytopenia; cancer; adenocarcinoma; leukaemia; myeloma; sarcoma; immune system disorder; acquired immundefriciency syndrome; AIDS; allergy; asthma; Crohn's disease; diabetes mellitus; gout; glomerulonephritis; Goodpasture's syndrome; thyroiditis; pancreatitis; hepatitis; multiple sclerosis; osteoporosis; Reiter's syndrome; rheumatoid arthritis; neurological disorder; epilepsy; stroke; dementia; Alzheimer's disease; Pick's disease; Huntington's disease; mood; anxiety; parkinson's disease; central nervous system disorder; mental disorder; schizophrenic disorder; amnesia; Tourette's disorder; transgenic animal; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                        17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                16-JAN-2001;
17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                         16-JAN-2001;
16-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; cDNA; 2311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYSGRYWTSWYKY 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRGKGYYWAGMWMKRYKRMYMYKMWWYKRKYSKCSWYCKMSYYASCMKSARKAGAKMCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TMGRCRYKKRSGMKRKCRRRRWGRMYRMRWKRYYMSARYTMRYCARKKYSYSAARKARCW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTGGTTGCTGCAGGCTGCGCCGGAGAACATAGTGATAAGGGATGTAACTTTCGATGAGAG
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; 2001US-0262760P.

2001US-0263063P.

2001US-0263066P.

2001US-0263069P.

2001US-0263070P.

2001US-0263074P.

2001US-0263074P.

2001US-0263074P.

2001US-0263079P.

2001US-0263329P.
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2001US-0261979P.
2001US-0261981P.
2001US-0262164P.
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2001US-0263131P.
2001US-0262599P.
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Panzer SR, L
Dam TC, Liu
Chang SC, Ge
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                                                                                                                                                                                                                                                                                                                                                                                                                        New purified secretory polypeptides and polynucleotides, useful in the diagnosis, study, prevention or treatment of diseases associated with decreased expression of functional secretory molecules, e.g. AIDS, cancer
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 260-261; 340pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE GENOMICS
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Liu TF, Harris
Gerstin EH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Altus CM,
Is B, Flores
Peralta CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC
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A, Marwaha R,
Lewis SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones
Chen
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leukaemia, myeloma or sarcoma, immune system disorder such as acquired immunodeficiency syndrome (AIDS), allergies, asthma, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, Hashimoto's thyroiditis, hepathtis, multiple sclerosis, osteoporosis, pancreatitis, Reiter's syndrome, autoimmune thyroiditis or rheumatoid arthritis, neurological disorders autoimmune thyroiditis or rheumatoid arthritis, neurological disorders such as epilepsy, stroke, Allzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease, other developmental disorder of the central nervous system, mental disorder including mood, anxiety or schizophrenic disorder, amnesia or Tourette's disorder. The polynucleotides may be used in hybridisation and amplification technologies, e.g. in assessing gene expression patterns, to develop a transcript image for a particular cell or tissue, or to create transgenic animals to model human disease. This sequence encodes a human secretory protein isolated in the invention

Sequence 2311 BP; 824 A; 325 C; 473 G; 689 T; 0 U; 0 Other;

Similarity

.94; DВ

6

Length 2311;

δ 밁 S 皮 Ş Query Match Best Local S Matches 80 345 **80**; GGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGGACGTCTTAACTTTTATTGCAGAG GACTATCAAATCATACAGATATTGTCAAA 699 CAGCTTAGTTTTCTTACTTTTTAAAATAATTTGGGTGATGTTTTAATCTAACTTGGÁCAT AGTTTAĀACĀĀTTTCCTTĀĀĀĀTTATTACTĀGCTGTTTTTTTTTCCTCĀTCĀTATTAĀA AGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAATCATATAAAA 5.3%; ilarity 53.7%; Conservative 0, Score 38.6; Di Pred. No. 0.94 0; Mismatches 69; Indels 0 Gaps 610 670 286 226 0

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RESULT 8
ADT96256/c
ID ADT9962
XX ADT962
XC ADT962
XX I6-DEC
XX UCOLON XX COLON XX
XX COLON XX ADT962
XX COLON XX ADT962
XX COLON XX ADT962
XX ADT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA sequence #1763.
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Colon cancer; T cell; tumour protein; C634S; C635S; C637S; C640S; C636S; humoral immune response; cellular immune response; cytostatic; immunostimulant; human; ss.

DNA organisation;

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RESULT 9
AAS29224/c
ID AAS29224 scandard; DNA; 7736
XX
AC AAS29224;
XX
                                                                                                                                                                                                                                                                                                                                                                                The invention relates to polynucleotide and polypeptide sequences CC associated with cancer, particularly colon cancer. Also disclosed are (i) CC an expression vector comprising the polynucleotide, (ii) a host cell CC transformed or transfected with the expression vector, (iii) an isolated antibody, or its antigen-binding fragment, which specifically binds to CC the polypeptide, (iv) a method of detecting or determining the presence CC of cancer in a patient, (v) a fusion protein comprising at least one of CC the polypeptides, (vi) an oligonucleotide that hybridises to the polypeptide sequence under highly stringent conditions, and (vii) a method of stimulating and/or expanding T cells specific for a tumour CC protein. The polypeptide specifically comprises the amino acid sequence CC of C634S, C635S, These polypeptides are encoded by the polynucleotide sequences, where both are capable of eliciting a humoral CC antibodies are useful for diagnosing, preventing or treating cancer, CC particularly colon cancer. The polynucleotide and polypeptide sequences are also useful in DNA strand invasion, antisense inhibition, mutational CC analysis, nucleic acid purification, isolation of transcriptionally cancer also useful for diagnosing, preventing or treating cancer. CC biomarkers. This sequence represents a human colon cancer associated CC cDNA. Note: The sequence data for this patent was obtained in electronic CC format directly from the USPTO web site at sequata.uspto.gov
                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jiang Y,
Carter D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acids and polypeptides capable of eliciting humoral and/or cellular immune response, useful for diagnosing, preventing or treating cancer, particularly colon cancer.
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07-FEB-2001; 2001US-0267382P.
11-MAY-2001; 2001US-0290322P.
12-JUL-2001; 2001US-0305265P.
16-AUG-2001; 2001US-0313077P.
                                                                                                                                                                                                                                                                                                                                                        Sequence 544 BP; 181 A; 70 C;
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                                                                                                                                                                                                          TCATTTGAATGTGTGAATTCAATACAGGCTATGTAAAATTTTTTACTAATGTCATTATTTT
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nilarity 57.5%;
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Smith CL,
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L, Durham M,
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26-JUL-2000;
26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2001; 2001WO-US001305
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                2000US-0229345P.
2000US-0229519P.
2000US-0230437P.
2000US-0231243P.
2000US-0231244P.
2000US-0231244P.
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2000US-0227182P.
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14-SEP-2000
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2000US-0246523P

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CC The present invention relates to the isolation of novel DNA-binding CC proteins (AAU18154-AAU18281), and CDNA and genomic sequences encoding for CC these proteins. DNA-binding proteins such as histones, chromo (chromatin CC organisation modifier) domain proteins, and y-box binding proteins may CC contribute to diseases resulting from aberrant DNA organisation and/or CC gene transcription. The sequences of the invention are useful in CC screening assays to identify antagonists and/or agonists that may enhance CC or block activities mediated by DNA-binding proteins. Blockers of DNA-CC binding proteins may be useful in treating disorders such as malignant CC diseases (e.g. cancer), autoimmune disorders (e.g. diabetes mellitus), CC rheumatic diseases (e.g. rheumatoid arthritis), genetic abnormalities CC (e.g. cystic fibrosis), infectious diseases (e.g. HIV) and neurological CC disorders (e.g. Alzheimer's disease). The polynucleotide sequences of the CC invention may also be used in gene therapy. AAS29158-AAS29239 represent CC genomic sequences encoding for novel DNA-binding proteins. Note: The Sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at fig. wipo.int/pub/published_pct_sequences
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06-DEC-2000

08-DEC-2000

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08-DEC-2000

11-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid molecules encoding human secreted chromosomal binding proteins, used in preventing, treating or ameliorating a disorder, Alzheimer's and Parkinson's diseases and cancers.
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; 2000US-02518479P.
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; 2000US-0251990P.
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Sequence 7736 BP; 1672 A; 1981 C; 2164 G; 1919 T; 0 U; 0 Other;

Query Match
Best Local Similarity
Matches 75; Conserv

Conservative

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5.2%; 54.7%;

Score 37.8; DI Pred. No. 2.9; 0; Mismatches

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                 TTGAAGCAACCGCACTA
                                         GAAGTACTCCACTCTCCCGAGTCTGCCTTTCCCTCATGGCCTCTGACCTCGCTCCCC
                                                        GGACCCCTCCTCCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCCTATCCCG
                                                                                       GTTCAGGGGATGGATGTAAAGCACACACACAGTTGTTCCCCCCACAGCCGCCCAGATGTG
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ID ABA16123;
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DT 23-JAN-20
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DE Human ner
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KW Human; now
KW immunosupi
KW antiparkii RESULT 10

standard; DNA;

ABA16123;

23-JAN-2002

Human nervous system related polynucleotide SEQ ID NO 8454.

Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;

1-JAN-2000; 2000US-0184064668666666666666666666666666666666	<pre>KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; KW antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; KW antiparasitic; cardiant; immune disorder; cardiovascular disorder; KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds. XX PN W0200159063-A2. XX PN W0200159063-A2. XX PT 16-AUG-2001. 2001WO-US001334.</pre>
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02-OCT 2000 02-OCT 2000 02-OCT 2000 03-OCT 2000 03-OCT 2000 03-OCT 2000 20-OCT 2000 20-OCT 2000 20-OCT 2000 20-OCT 2000 08-NOV 2000 09-DEC 2000 09-DEC 2000 08-DEC 2000 08-DEC 2000 08-DEC 2000 08-DEC 2000 08-DEC 2000 08-DEC 2000 08-DEC 2000	
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                     hyperproliferative disorder; cancer; renal disorder; arrhythmia; acute glomerulonephritis; cardiovascular disorder; respiratory diso Goodpasture's syndrome; neurological disorder; Alzheimer's disease; Parkinson's disease; endocrine disorder; Addison's disease; reproductive system disorder; endometriosis; infectious disease;
                                                                                                                                                     Human; DNA-binding protein; B cell immunodeficiency; autoimmune disorder; severe combined immunodeficiency; rheumatoid arthritis; Crohn's disease; diabetes mellitus; allergy; asthma; inflammatory condition; thrombosis; graft-versus-host disease; blood-related disorder; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.
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05-JAN-2001; 2001US-0259678P.
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                                                                                                       disorder;
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nd healing
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  14-AUG-2000

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14-AUG-2000

22-AUG-2000

01-SEP-2000

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07-SEP-2000

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09-SEP-2000

29-SEP-2000

29-SEP-2000

09-SEP-2000

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01-SE
                     Novel DNA-binding protein useful for diagnosis, prognosis, prevention treatment of immune, hyperproliferative, respiratory, cardiovascular, reproductive, endocrine, gastrointestinal and neurological disorders.
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                                                                                                                                                                                   Rosen
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RUBEN S
BARASH S
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gastrointestinal disorder; multiple sclerosis; gene therapy; ds
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2000US-022934P
2000US-022934SP
2000US-022934SP
2000US-0229509P
2000US-0231413P
2000US-0231413P
2000US-023427AP
2000US-023427AP
2000US-023499P
2000US-023499P
2000US-023636P
2000US-023636P
2000US-023636P
2000US-023636P
2000US-023636P
2000US-023637P
2000US-023637P
2000US-0236379
2000US-0236399
2000US-0237039P
2000US-0237039P
2000US-0237039P
2000US-0241966P
2000US-0241966P
2000US-0241969P
2000US-0241869P
2000US-0241869P
2000US-0241869P
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2000US-0241869P
2000US-0241869P
2000US-0241869P
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2000US-0225267P.
2000US-0225268P.
2000US-0225270P.
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2000US-0225757P
2000US-0225758P
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Barash
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and

2000US-0180628P 2000US-0184664P

2000US-0198123P 2000US-0186350P. 2000US-0189874P.

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RESULT 12
ADC25486/c
ID ADC254
XX
AC ADC254
XX
AC ADC254
XX
OT 18-DEC
XX
PHUMAN
XX
PEXTRAC
KW EXTRAC
KW neurop
KW cardio
KW respir
KW nootro
KW neural
KW neural
KW muscul
KW pulmon
KW Jene
XX
OS Homo s
XX
VS US2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a new DNA-binding protein. The invention CC is useful in treating, preventing, diagnosing and/or prognosing communodeficiencies (e.g. B cell immunodeficiencies, severe combined immunodeficiencies), autoimmune disorders (rheumatoid arthritis, multiple collectosis, diabetes mellitus), allergic reactions and conditions (e.g. calcrosis, diabetes mellitus), allergic reactions and conditions (e.g. casthma), inflammatory conditions, graff-versus-host disease, blood-crost (e.g. cancer), renal disorders (e.g. acute glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders (c.g. acute glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders (c.g. arrhythmia), respiratory disorders (c.g. arrhythmia), respiratory disorders (c.g. Alzheimer's (disease, parkinson's disease), endocrine disorders (e.g. Alzheimer's (disease), reproductive system disorders (e.g. endometriosis), infectious disease), reproductive system disorders (e.g. endometriosis), infectious disease (e.g. viral, bacterial or fungal infections) and casteriorite to stimulate neuronal growth and treat, prevent, and/or diagnose cuseful to stimulate neuronal growth and treat, prevent, and/or diagnose neuronal damage which occurs in certain neuronal disorders or neuro-condegenerative conditions. The present nucleic acid sequence represents a protein genomic DNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed control of the printe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                     Extracellular matrix protein; cytostatic; antibacterial; virucide; neuroprotective; gynaecological; gastrointestinal-Gen; cardiant; cardiovascular-Gen; nephrotropic; antiinflammatory; muscular-Gen; respiratory-Gen; immunosuppressive; cerebroprotective; vasotropic; nootropic; antiallergic; cancer; bacterial infection; viral infection; neural disorder; immune system disorder; blood disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; pulmonary disorder; proliferative disorder; human; gene therapy; ss
                                  07-MAR-2002; 2002US-00091483.
                                                                     13-MAR-2003.
                                                                                                       US2003049650-A1
                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  Human cDNA from extracellular matrix gene 78 #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC25486;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC25486 standard; cDNA; 7736 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 333; 225pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http.seqdata.uspto.gov/sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5124
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Pred. No. 2.
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                                                                                                                                                                                         gene therapy; ss;
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29-SEP-2000
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
12-AUG-2000;
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23-AUG-2000;
01-SEP-2000;
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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08-SEP-2000;
12-SEP-2000;
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08-SEP-2000;
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08-SEP-2000;
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14-AUG-2000
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31-JAN-2000; 2000US-0179065P

2000US-0233065P. 2000US-0234223P. 2000US-0234274P. 2000US-0234997P.

2000US-0231968P. 2000US-0232397P. 2000US-0232398P. 2000US-0232399P. 2000US-0232400P.

2000US-0231242P. 2000US-0231243P. 2000US-0231244P. 2000US-0231413P. 2000US-0231414P.

2000US-0229344P. 2000US-0229345P. 2000US-0229509P. 2000US-0229513P.

2000US-0230437P. 2000US-0230438P.

2000US-0224519P. 2000US-0225213P. 2000US-0225214P. 2000US-0225266P. 2000US-0225267P.

2000US-0218290P. 2000US-0220963P.

2000US-0224518P 2000US-0220964P

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13-OCT-2000

20-OCT-2000

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20-OCT-2000

01-NOV-2000

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09-NOV-2000

017-NOV-2000

17-NOV-2000

17-N
          New DNA-binding treating and/or
                                                            WPI; 2003-605749/57.
P-PSDB; ADC25241.
                                                                                                              Ruben SM,
                                                                                                                                                                           2000US-0244617P.
2000US-0246474P.
2000US-0246477P.
2000US-0246477P.
2000US-0246524P.
2000US-0246524P.
2000US-0246528P.
2000US-0246528P.
2000US-0246532P.
2000US-0246532P.
2000US-0246611P.
2000US-0246611P.
2000US-0246611P.
2000US-0246611P.
2000US-0249208P.
2000US-0249218P.
2000US-024921P.
2000US-02511B.
2000US-025199.
2000US-025199.
2000US-0254097P.
2000US-0254097P.
2000US-0259494.
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2000US-0237039P.
2000US-0237040P.
2000US-0239935P.
                                                                                                                                                GENOME
proteins and gene encoding them, useful for diagnosing, preventing e.g. neurological, inflammatory, infectious,
                                                                                                                                                SCI
                                                                                                              Barash SC;
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RESULT 13
ABV04394
ID ABV04394
XX ABV04
AC ABV04
XX Human
XX Human
XX Human
XX Human
XX Pharm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC binds specifically to the protein, diagnosing a pathological condition or susceptibility to a pathological condition (comprising determining the presence or absence of a mutation in the nucleic acid and diagnosing a CC condition based on the presence or absence of the mutation), diagnosing a CC pathological condition or susceptibility to a pathological condition (comprising determining the presence or amount of expression of the protein in a biological sample and diagnosing a condition based on the CC presence or amount of expression of the protein), preventing, treating or CC ameliorating a medical condition by administering the nucleic acid or protein to a mammalian subject, identifying a binding partner to the CC protein to a mammalian subject, identifying a binding partner to the corresponding to the cDNA sequence, and identifying an activity in a biological assay (comprising expressing the nucleic acid in a cell, isolating the supernatant, detecting an activity in a biological assay and identifying the protein in the supernatant having the cell acids and proteins display the following activity). The nucleic acids and proteins display the following the proteins display the following contributes Cytostatic, antibacterial, Virucide, Neuroprotective,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local :
                                                           17-FEB-2000;
16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                             20-FEB-2001; 2001WO-US005171
                                                                                                                                                                                                                                                                                                                                                                                                          WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human prostate expression marker cDNA 4385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV04394 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5184 GTTCAGGGGATGGATGTAAAGCACACACAGTTGTTCCCCCCACAGCCGCCCAGATGTG
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                                                       ; 2000US-0183319P.
; 2000US-0189862P.
; 2000US-0207454P.
; 2000US-0211314P.
; 2000US-0211314P.
; 2000US-0255281P.
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC

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RESULT 14

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Best Local Similarity
Matches 56; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cancer has metastatized in a patient; (f) assessing the prostate cancer has metastatized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient in the aggressiveness or indolence of prostate cancer in a patient.
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nilarity 64.4%;
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for treating, preventing and/or prognosing the musculoskeletal system including musculostesting and detection e.g. diagnosis. musculoskeletal

Claim 1; SEQ IJ NO 819; 781pp + Sequence Listing; English.

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies the invention relates to (ABB03087-ABB04109) assoc for

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RESULT 15
ABX58465/c
ID ABX584
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KW Ceardio
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31-JAN-2000;
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28-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene; ss; musculoskeletal system antigen; cancer; metastasis; re-vascularisation; thrombosis; arteriosclerosis; miscral content; cardiovascular condition; wound; injury; burn; angiogenesis; ulcer; post-operative tissue repair; limb regeneration; neuronal growth; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; along related complex advantages.
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29-SEP-2000

20-OCT-2000

20-OC
      The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers, stimulates angiogenesis and limb regenerative issue repair, and ulcers, stimulates angiogenesis neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or neurotyte.
                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer.
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SUMMARIES

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ORIGIN

ALIGNMENTS

	FEATURES BOURCE	TITLE JOURNAL	SOURCE ORGANISM REFERENCE AUTHORS	RESULT 1 AQ874584/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS
/OUR LEAR OR COLLEGE OF THE COLLEGE		desEtages, S.A., Cheung, KH., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M. Large-Scale Analysis of the Yeast Genome by Transposon Tagging and Gene Disruption (1999) Contact: Xumar A	Saccharomyces cerevisiae (baker's yeast) Saccharomyces cerevisiae Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces. 1 (bases 1 to 434) Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A.,	AQ874584 V111B3 mTn-3xHA/lacZ Insertion Library, strain Y2278 Saccharomyces cerevisiae genomic 5', genomic survey sequence. AQ874584 AQ874584.1 GI:6286828 GSS.

Query Match

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L Submitted (07-58P-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

8 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen

yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces

exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces

lactis var. lactis, Kluyveromyces thermotolerans, kluyveromyces

lactis var. lactis, Kluyveromyces marxianus var. marxianus, pichia

angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,

Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to

5 kb were prepared and both extremities were sequenced. See

keywords for description of this sequence and for the sequence of

the other extremity of this insert.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B., Malperruy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissenbach, J. Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNS06GVN 927 bp DNA linear GSS 30-NOY-200 T3 end of clone AS0AA007G06 of library AS0AA from strain CLIB 533 of Saccharomyces bayanus, genomic survey sequence.
AL398217 AL398217.1 GI:12151528
                                                                                                                                                                                                                                                                                                                    Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                         Genomic exploration of the hemiascomycetous yeasts: 5. Saccharomyces bayanus var. uvarum FEBS Lett. 487 (1), 37-41 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bon, E., Neuveglise, C., Aigle, M. and Durrens, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 927)
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                                                                                                                                          Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Drosophila melanogaster
Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Phydroidea; Drosophilidae; Drosophila.
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                              GSS.
                                                        Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                   CNS0090X Page 100 DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR19021 of RPCI-98 library from Drosophila melanogaster (fruit fiv) 5021 of Process Research Proce
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/clone="ASOAA007G06"
/clone_lib="ASOAA"
/note="end : T3"
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Pred. No. 6.7e-29;
0; Mismatches 107;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 WTGAAATAAGAGTTTTTATGCTTCTKAAAWGCTGAAATACATWTTCKDWKKGKKGKCSGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      522 TAGTGATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTA 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 462 ATTIGGGTAAGCCCCTTTCTGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCGCGGAGAACA 521
                                                                                                               Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus.

1 (bases 1 to 1055)

Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R. Gallus gallus BAC End Reads
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                          CH261-136H21_Sp6.1 CH261 Gallus gallus
                      Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                           Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                          genomic survey sequence. CC252581
Insert Length: 182000
                                                                                              Contact: Richard K. Wilson
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/mol type="genomic DNA"
/mb type="genomic DNA"
/db xref="taxon:7227"
/clone="BACR19021"
/clone_lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="end : TET3"
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  Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    614 GAGACCACCCTGTAGAGGGAGAATAATATGGAGGGAAAAATATGAGTGAGAAGGGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               674 GTCCCCCTCTATTTTCATATAGTGTCTGATTCCTGCAGAGCTGGAGATAATAGGTGGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83;
                                                                                                                                                                                                                                   collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome
BACN37F10 of DrosBAC library fr
fly), genomic survey sequence.
AL108171
AL108171.1 GI:5628475
GSS.
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High
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: Sp6 ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                              - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNS017KX
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/clone_lib="CH261"
/clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Femalle Chicken library - For library and clone
ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
                      /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
                                                                     /mol_type="genomic DN
/db_xref="taxon:7227"
/clone="BACN37F10"
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survey sequence SP6 end of BAC
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                                                                                                                                                                                                                                                                                                                                                                                              - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                               Similarity
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genome survey sequence SP6 end of BACN08K14 of DrosBAC library from Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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AACTATGGDTAAMTTTAWWAATTTTHTAAAGGGAAGAWTTWTTTTTTAAGKGGCCTWT
                         AATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCTTAACTTTTATTGCAGAGGACTAT 676
                                                                 AVYAWRGGGGAATSGMGGAYCKGWAWTTTYYWWAWTWTTTTTWWTTTKGWAAGMAAMSAA
                                                                                                  AGCAAGCGGAAAAAAACTATGGCTAGCTGGGAGTTGTTTTTCAATCATATAAAAGGGAGA
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                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic survey
                                                                                                                                                                                                                             /clone="BACN08K14"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                       5.8%; Score 41.6; DE 42.2%; Pred. No. 1.7; ative 25; Mismatches
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                                                                                                                                                                        Length 1101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
Library was constructed by R. Haywood. DNA sequencing by:
Washington University Genome Sequencing Center For information
obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang, K., Cole, R., Chakrabarti, D., Haywood, R., Clifton, S., Pape, D., Marra, M., Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Jentes, E., Ronko, I., Tsagaraishvili, R., Belaygorod, L., Franklin, C., Carr, L., Grow, A., Maguire, L., Richey, J., Wadkins, J., Kennedy, S., Levinso, D., Waterston, R., Wilson, R. and Sibley, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: L. David Sibley
WashU Plasmodium EST Project
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                          Similarity
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Plasmodium falciparum 3D7
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium
1 (bases 1 to 436)
IGTTTATTACATATGAAATTTCGATATTATTCCTTTGGAAGGATAATTTTGTGGGATAAA 196
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                                                       TTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTC
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                                                                                                                    Conservative
                                                                                                                                                                                                                               /note="Vector: pBluescript SK plus; Site 1: EcoRI; Site 2: XhoI; The library was constructed by R Haywood. cDNAs were synthesized from ganetocyte poly(A) + RNA by oligo d(T) priming, size-selected and directionally cloned into the EcoRi (5' end) to XhoI (3' end) sites of the Uni-ZAP XR lambda vector (Stratagene). The primary library was mass excised as phagemid using the ExAssist helper phage (Stratagene). Clones were mass excised using the ExAssist helper phage (Stratagene), the phagemids were precitptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DHIOB cells. Clone Availability: David Sibley, Washington University."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="gametocyte (stage III-V)"
/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/clone_lib="Plasmodium falciparum 3D7 gametocyte cDNA
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/db_xref="taxon:36329"
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                                                                                                                                       5.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Raccollaboration with the European Drosophila Genome Project (EDGP) - Determination with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC | Library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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AL098379
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Drosophila melanogaster
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                                                                                                                                    GAGAAATTGTTGCTCACTATGTGACAGTTTTCTGGGACGTCTTAACTTTTATTGCAGAGGA 672
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GKRGDGDRKDKGTGGDGDSKAKGDRAWAWRAKATRAAAAAAATAAKAT
                                            KDWDWKDADTKAGRKRGWGKKGGWKKTTKTKKKKTDKTKTGTDTKWGWKDKWTDKKRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : SP6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institude, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
KOyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
primers
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BH572702
BH572702.1 GI:17824541
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                                                                BOGTD44TF BOGT Brassica oleracea
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LIBRARY
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus molossinus"
|mol type="genomic DNA"
|sub specise="molossinus"
|db_xref="taxon:57486"_____
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="MSMg01-443E08.TJ"
/sex="male"
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Pred. No. 2.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            578 GCTAGCTGGGAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGAC
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 791)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                BI255759
BI255759.1 GI:14809497
                                                                                                                                                                                                                                                      602977180F1 NIH_MGC_12 Homo sapiens
                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                              mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: TF
Class: sheared ends.
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Brassica oleracea
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DNA is from a doubled haploid provided by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
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    Library Preparation: Life Technologies, Library Arrayed by: Incyte Genomics, In
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="BOGT"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
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/db_xref="taxon:3712"
/clone="BOGTD44"
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/mol_type="genomic DNA"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryqii; Neopteryqii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopteryqii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                          Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of reshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
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                                                                                                                                                                                                                                                                                           Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000) 20296633
                                                                                                                                                                                                                                                                                                                                                                                              Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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GSS; genome survey sequence.
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11298 row: o column: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NIH_MGC_12"
/note="organ: cervix, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.4 kb. Library prepared by Life
Technologies."
1 to
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:5122410"
/tissue_type="cervical carcinoma
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Best Local Similarity
Matches 59; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
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Direct Submission

Direct Submission

Submitted (12-AFR-2000) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web: www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG628729 366 bp mRNA linear EST cC-esfictEL23G13d1 Tomato flower library from a mixture developmental stages Lycopersicon esculentum cDNA clone cC-esfictEL23G13d1, mRNA sequence.
                                                                                                                                                                                                                                                 Tel: 607 255 7886
Fax: 607 255 6683
Email: rv19@cornell.edu
                                                                                                                                                                                                                                                                                                             Contact: Rutger S. van der Hoeven
Cornell University
252 Emerson Hall, Ithaca, NY 1485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum (tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG628729.1 GI:13680202
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                                                                                                                                                                                                                                     sequence.
/db_xref="taxon:4081"
/clone="C_eeficLEL23G13d1"
/tissue type="developing flower buds and open flowe:
/tissue type="developing flower buds and open flowe:
/dev_stage="4-8 week old plants"
/lab_host="XLOIR"
/clone_lib="Tomato flower library from a mixture of developmental stages"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                     cultivar="E6203"
                                                                                                                                                                         organism="Lycopersicon esculentum'
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU077905
AU077905 Rice shoot Oryza sativa (japonica clone S5033_8Z, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Takuji Sasaki
National Institute of Agrobiological Re
Rice Genome Research Program, Kannondai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice cDNA from etiolated shoot 
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 518)
Yamamoto, K. and Sasaki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 81-298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AU077905.1 GI:5667645
                                                                                                                                                                                                                                                                                                                                                                                                Email: tsasaki@abr.affrc.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 81-298-38-7468
                                                                                                                                                                                                                                                                                                                                                                                                                                               305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3hrhartoideae; Oryzeae; Oryza.
 TAATAACA 722
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                                                                                                                                                                                                                                                                          /organism="Oryza sativa (
/mol type="mRNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="S5033_8Z"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBK_CMV; Site_1: EcoRI; Site_2: XhoI;
Flowers and flower buds were collected from greenhouse
grown plants and used for library construction (CLEL)
                                                                                                                                                                                                                           /dev_stage="ETiolated shoot (8 days (/clone_lib="Rice shoot"
/note="Etiolated shoot (8 days old)"
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                                                                                                                                                                  Score 40; DB
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Pred. No. 4.1;
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AUTHORS
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SOURCE
ORGANISM
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AZ541311
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                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                          Query Match 5.5%; Score 40; DB 8; Length 845; Best Local Similarity 55.9%; Pred. No. 4.8; Matches 76; Conservative 0; Mismatches 60; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Entamoebidae; Entamoeba.

Eu 1 (bases 1 to 845)

E 1 (bases 1 to 845)

Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica

HM1: MSS sheared DNA library

LU Dupublished (2000)

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

Department of Eukaryotic Genomics

Department of Eukaryotic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 3543

Email: bjloftus@rtigr.org

Clones are derived from the Entamoeba histolytica HM1: IMSS sheared
                                                                                                                                               527 TTATGAAAAATAATAT 542
                              708 AGACTAATAATAACAT 723
                                                                                                      467 AGTTTCTTAATTTAATAGTATAGAAATATTAATCAATAGATGCTTTTTCTAACAAAAATT 526
                                                                                                                                                                                                            407 AATTAATTAAATAAAATATCATTTTGAATAATTTTTTATTGTTAATTGACAGAATCTGAA
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AZ541311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 42
High quality sequence stop: 612
Location/Qualifiers
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Entamoeba histolytica
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Class: shotgun
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                                                                                                                                                                                                                                                  AGTTGTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTTCTGGG 647
                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="Entamoeba histolytica Sheared DNA"
/clone lib="Entamoeba histolytica Sheared DNA"
/notee="Vector: pHOS1; Site 1: BST I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mol_type="genomic DNA"
strain="HM1:IMSS"
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Search completed: February 7, 2005, 23:17:23 Job time: 3219 secs

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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723
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	34. 34.	444	4444		723 723 720.4 720.4 37.8 37.8 35.8	Score
4.7 4.7	4.7	4.7 4.7		4444	100.0 100.0 100.0 99.6 5.2 5.2	Query Match
232547 313 502	0.01	105189 1876 14205	601 601 51723 51723	212449 72992 98962 102884	723 11427 13073 13073 7218 4989 11440 16662 815	Length
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US-09-949-016-16603 US-09-513-999C-35864 US-09-621-976-18891	-09-949-	-09-949-016-1302 -09-469-242-3 -09-949-016-1619	US-09-949-016-26160 US-09-949-016-183245 US-09-949-016-12152 US-09-949-016-16991	-09-949-016-1541 -09-949-016-1759 -09-949-016-1413 -09-949-016-1413	US-09-743-194-2 US-09-743-194-24 US-09-743-194-20 US-09-743-194-20 US-08-232-463-14 US-08-232-463-14 US-09-949-016-17442 US-09-949-016-16850 US-09-369-247-15	ID
e 16603, e 35864, e 18891,	Sequence 13631, A Sequence 13602, A	e 13029, e 3, App e 16196,	01-	15419, 17592, 17133, 14133,	Sequence 2, Appli Sequence 24, Appl Sequence 20, Appl Sequence 30, Appl Sequence 14, Appl Sequence 17445, A Sequence 17445, A Sequence 17445, A Sequence 16850, A Sequence 15, Appl	Description

										
Qy	D Qy	Db Qy	Db Qy	ОУ	Qу	D Qy	Query Ma Best Loc Matches	RESULT 1 US-09-743-194- Sequence 2, Patent No. 6 GENERAL INCO GENERAL INCO APPLICANT: CURRENT FIL. AUMBER OF S. SOFTWARE: SOFTWARE: SOFTWARE: APPLICANT: A		00 000 000 0000 0000 0000 0000 0000 00
361 GTCTC	301 GGTAA 301 GGTAA	241 GCACT 241 GCACT	181 CTCCC	121 GGGGG 121 GGGGG	61 ACCAT	1 CTTTC 1 CTTTC	tch al simil 723; C	-194-2 2 Applic 3 2 Applic INFORMATIC INFORMATIC OAKIE DF INVENTIO SFERENCE: 3 F APPLICATIO OF SEC ID OF FILING DA OF SEC ID O		
GATAATAGAA 	CGGCACCGTG	ATGACTAAATG ATGACTAAATG	CGCACGATTT	CTAAGAAGTC	'AAAGAGCAAA AAAGAGCAAA	GATTAGCACG GATTAGCACG	100 rity 100 nservative	ation N: N: Car Y: Car N: Con N: CON TE: NOS: 3 N Ver.		.7 4818 .6 77851 .6 77867 .6 77940 .6 312470 .6 336024 .6 336024 .6 784019 .6 828152 .6 828152 .6 828153 .6 828153 .6 828153 .6 828153 .6 98567 .5 100567 .5 301828 .5 301828
TAATAAGCGCA 	GCTCGGAAACG GCTCGGAAACG	GGTGCTGGACA GGTGCTGGACA	CTTCCTTTCATA CTTCCTTTCATA	ATTCACTTTCT	GCGATACCTACT	CACACACATCA CACACACATCA	0%; Score 0%; Pred. 0; Mis	7743194 ions and ling Nucl US/09/743 11-08	ALIG	3 US-08-8 4 US-09-9 5 US-09-9 6 US-09-9
GTCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCGGCGCCGCCGCTTTCCCA	GGTDACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTAGAACAGGGGCTAC 	GCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGTGTGTATCTCACAG 	TCCCCGCACGATITCTTCCTTTCATATCTTCCTTTTATTCCTATCCCGTTGAAGCAAC 	GGGGGCTAAGAAGTCATTCACTTTCTTTTCCCTTCGCGGTCCGGACCCGGGACCCCTCCT 	accataaagagcaaagcgatacctacttggaaggaaaaggagcacgcttgtaaggggga 	CATAGACTGCGTC	723; DB 4; No. 1.9e-229 matches 0;	hods U Acid	ALIGNMENTS	B-817-926-27)9-949-016-13212)9-949-016-13212)9-949-016-1325)9-949-016-1259)9-949-016-1207)9-949-016-1237)9-949-016-1237)9-949-016-1237)9-949-016-12777)9-949-016-1777)9-949-016-1777)9-949-016-17576)9-949-016-17576)9-949-016-17576)9-949-016-17576)9-949-016-11750)9-949-016-11750)9-949-016-11750)9-949-016-11750
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CGTTTCCCA 420	AGGGGCTACA 36 AGGGGCTACA 36	TCTCACAGT 300	GAAGCAACC 240 GAAGCAACC 240	ACCCCTCCT 18	AAGGGGGAT 120 AAGGGGGAT 120	CACTACGGAAAA 60 CACTACGGAAAA 60	0; Gaps	nces for Yeast		nce 27, Appl nce 12508, A nce 13211, A a nce 13212, A nce 13210, A nce 12509, A nce 12509, A nce 1403, A nce 12373, A nce 12373, A nce 12373, A nce 60957, A nce 60957, A nce 17576, A nce 17576, A nce 17576, A nce 16934, A nce 16934, A nce 13969, A nce 13969, A

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Best Local Similarity
Matches 723; Conserv
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Patent No. 6716601
GENERAL INFORMATION:
APPLICANT: Belifield, Graham
APPLICANT: Oakley, Caroline
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for TITLE OF INVENTION: Controlling Nucleic Acid Expression in Yeast CURRENT APPLICATION NUMBER: US/09/743,194
CURRENT APPLICATION NUMBER: US/09/743,194
CURRENT FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
cpc TD NO 24
                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 24
LENGTH: 11427
                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
-09-743-194-24
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                                                     CTCCCCGCACGATTTCTTCCTTTCATATCCTTCCTTTTATTCCTATCCCGTTGAAGCAACC
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APPLICANT: Oakley, Caroline
ITITLE OF INVENTION: Compositions and Methods
ITITLE OF INVENTION: Compositions and Methods
ITITLE OF INVENTION: Controlling Nucleic Aci
IFILE REFERENCE: 3526.82543
CURRENT APPLICATION NUMBER: US/09/743,194
CURRENT FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 13073
TYPE: DNA
ORGANISM: Saccharomyces cerevisiae
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Matches
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Patent No. 6716601
GENERAL INFORMATION:
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                                                                                     CTCCCCGCACGATTTCCTTCCTTTCATATCTTCTTATTCCTATCCCGTTGAAGCAACC
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RESULT 4
US-09-743-194-30
; Sequence 30, Application US/09743194
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Best Local S
Matches 721
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APPLICANT: Oakley, Caroline
TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for
TITLE OF INVENTION: Controlling Nucleic Acid Expression in Yeast
FILE REFERENCE: 3526.82543
CURRENT APPLICATION NUMBER: US/09/743,194
CURRENT FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
LENGTH: 850
TYPE: DNA
CONTROLLED OF TARGET PARAMETERS OF SEQ ID NO 30
LENGTH: 850
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            CTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATCCCGTTGAAGCAACC
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Conservative
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Pred. No. 1.5e-228;
0; Mismatches 1;
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                                                                                                                                                                                 CITY: Alexandria
STATE: VA
STATE: VA
COUNTRY: USA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
PILING DATE: EP 91 114 300.6
APPLICATION NUMBER: EP 91 114 300.6
PILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                        APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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                                                                                                                                                                                                      Version
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; ORGANISM: Human US-09-949-016-17445
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                                                      SEQ ID NO 17445
LENGTH: 4989
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 17445, Application US/09949016 Patent No. 6812339
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                                                                                                                           PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                   FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                             APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                           NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                       TYPE: DNA
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LENGTH: 7218 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-09-949-016-17442
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Best Local S
Matches 75
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17442
LENGTH: 11440
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17442, Application US/09949016 Patent No. 6812339
                                                                                                                                                                         Sequence 16850, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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; Pred. No. 0.22;
0; Mismatches
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Pred. No. 0.36,
0; Mismatches
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012

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CURRENT APPLICATION NUMBER: US/09/369,247
CURRENT FILING DATE: 1999-08-05
EARLIER APPLICATION NUMBER: 60/074,118
EARLIER APPLICATION NUMBER: 60/074,157
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,137
EARLIER APPLICATION NUMBER: 60/074,137
EARLIER APPLICATION NUMBER: 60/074,341
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-02-09
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NUMBER OF SEQ ID NOS: 172
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 815
                                                                                                                              Query Match
Best Local (
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SEQ ID NO 16850
LENGTH: 16662
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Best Local Similarity
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                                                                                                                                                                                  FEATURE:
NAME/KEY: SITE
LOCATION: (794)
OTHER INFORMATION: n equals a,t,g, or c
-09-369-247-15
                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE: RAME/KEY: SITE LOCATION: (406) OTHER INFORMATION: n equ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/074,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
ATMIR OF INVENTION: 44 Human Secreted Proteins
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                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 TCCCTTCGCGGTCCGGACCCCGGGACCCCTCTCTCCCCCGCACTTTCTTCCTTTCATAT 208
                                    665 TATCCTGTTATTTAAATGTGAACATTTATTGTACATTCAGTGAGTTATAGTGTTAATAGT
                                                                       594 TTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGGGACGTCT
similarity 55.1%;
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                                                                                                        Score 35.8; DB Pred. No. 0.34; O; Mismatches
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Pred. No. 1
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                                                                                                                                           DB 4; Length 815;
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                                                                                                            57; Indels
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US-09-949-016-16144
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US-09-949-016-16144
                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: VENTER, 7: Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16144
LENGTH: 191433
                                                                                                                   NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15419
LENGTH: 212449
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Best Local Similarity
Matches 60; Conserv
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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PRIOR FILING DATE: 2000-10-20
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
OTHER INFORMATION: n =
                  NAME/KEY: misc_feature
LOCATION: (1)...(212449)
                                                            FEATURE:
                                                                             ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 GACCCGGGACCCCTCCTCCCCGCACGATTTCTTCCTTTC 204
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ilarity 59.4%;
Conservative (
  A,T,C
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Pred. No. 12;
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OF DETECTION AND USES THEREOF
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US-09-949-016-14133/c
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                                                       CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-08
PRIOR FILING DATE: 2000-09-08
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                         Sequence 14133, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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LENGTH: 72992
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APPLICANT: VENTER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17592, Application US/09949016 Patent No. 6812339
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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SEQ ID NO 14133
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/99/949,016
                                                                                                                                                                                                                                                  APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                   NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 ATTTCTTCCTTTCATATCTTCCTTTATTCCTATCC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 AGTCATTCACTTTCTTTTCCCTTCGCGGTCCGGACCCGGGACCCCTCCTCTCCCCGCACG 191
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Pred. No. 13;
0; Mismatches
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OF DETECTION
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 17100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (1)...(98962)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-14133
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; ICCATION: (1)...(102884)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-17100
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Best Local Similarity
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: CL001307
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ORGANISM: Human
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ORGANISM: Human
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                                                                                                                                   78525 TCCTGGGGAGGCAGTGGGGTGGGTGAGTGGGGGAGGGCCTTCACCACCCCCAACATTT
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US-09-949-016-26160/c

Sequence 26160, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE; CL001307

CURRENT APPLICATION UNMBER: 05/241,755

PRIOR TILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH: 601

TYPE: DNA

GORANISM: Human

US-09-949-016-26160
Search completed: February 7, 2005, 23:20:25 Job time : 180 secs
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                                                                                                                                                                           349 ACTGGCCAAGAAACAGAGTAATGAGGCAAAAGAGGTGGTGATGAAGAAYCTTATATATGT 290
                                                                                                                                                                                                                                                            289 CATT 286
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Perfect score:
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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/ cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/US08_NEW_CUB.seq:*
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SUMMARIES

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Result
723 723 720.4 497.4 41 41 41 41	Score
100.0 100.0 100.0 99.6 68.8 5.7 5.7 5.7 5.7	Query Match Length
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166711188	DB
US-10-776-213-2 US-10-776-213-24 US-10-776-213-30 US-10-776-213-30 US-10-451-467A-317 US-10-451-457A-317 US-10-123-155-198 US-10-146-731-198 US-10-140-72-198 US-10-141-761-198 US-10-141-761-198 US-10-142-885-198 US-10-142-885-198	ID
Sequence 2, Appli sequence 20, Appl sequence 20, Appl Sequence 30, Appl Sequence 31, App sequence 198, App	Description

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e 6815	16893	168936	4593,	Sequence 2883, Ap	1976,	e 819,	819,	Sequence 94399, A	25183,		e 2518	Sequence 25182, A	Sequence 106895,	e 1068	Sequence 106895,	1068	96559,	4385		ω		29921,	1775		136	20, 1	198,	198,	e 198,	,8	8	,8	

ALIGNMENTS

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121 GGGGCTAAGAAGTCATTCACTTTCTTTTCCCTTCGCGGTCCGGACCCCGGGACCCCTCCT 180	121 GGGGCTAAGAAGTCATTCACTTTCTCTTTTCCCTTCGCGGTCCGGACCCCGGGACCCCTCCT 180	61 ACCATAAAGAGCAAAGCGATACCTTAGGAAGGAAAAGGAGCACGCTTGTAAGGGGGAAT 120	61 ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGGAT 120	1 CTTTCGATTAGCACGCACACACATCACATAGACTGCGTCATAAAAATACACTACGGAAAA 60	1 CTTTCGATTAGCACGCACACACACACATAGACTGCGTCATAAAAATACACTACGGAAAA 60	Query Match 100.0%; Score 723; DB 18; Length 723; Best Local Similarity 100.0%; Pred. No. 5.5e-217; Matches 723; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SSULT 1 1:10-776-213-2 Sequence 2, Application US/10776213 Sequence 2, Application US/10776213 Publication No. US20040142478A1 Publication No. US20040142478A1 GENERAL INFORMATION: APPLICANT: AstraZeneca AB TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for Controlling Nucl TITLE OF INVENTION: Acid Expression FILE REFERENCE: 3526.82543 CURRENT APPLICATION NUMBER: US/10/776,213 CURRENT APPLICATION NUMBER: US/10/776,213 CURRENT FILING DATE: 2004-02-12 NUMBER OF SEQ ID NOS: 32 SOFTWARE: PAtentIn Ver. 2.0 SEQ ID NO 2 LENGTH: 723 TYPE: DNA ORGANISM: Saccharomyces cerevisiae -10-776-213-2

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RESULT 2
US-10-776-213-24
; Sequence 24, Application US/10776213
; Publication No. US20040142478A1
; Publication No. US20040142478A1
; GENERAL INFORMATION:
APPLICANT: ASCTAZENECA AB
; TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for Controlling |
FILE REFERENCE: 3526.82543
; CURRENT APPLICATION NUMBER: US/10/776,213
; CURRENT APPLICATION NUMBER: US/10/776,213
; CURRENT FILING DATE: 2004-02-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 24
; LENGTH: 11427
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                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Saccharomyces
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                ACCATAAAGAGCAAAGCGATACCTACTTGGAAGGAAAAGGAGCACGCTTGTAAGGGGGGAT 120
                                                                 CTTTCGATTAGCACGCACACACATCACATAGACTGCGTCATAAAAATACACTACGGAAAA 60
                                                 CTTTCGATTAGCACGCACACACATCACATAGACTGCGTCATAAAAATACACTACGGAAAA
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                                                                                                     100.0%; Score 723; DB 18; ilarity 100.0%; Pred. No. 2.5e-216; Conservative 0; Mismatches 0;
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                                                                                                                            Length 11427;
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RESULT 3
(S-10-776-213-20
(WS-10-776-213-20
(Sequence 20, Application US/10776213
); Sequence 20, Application US/10776213
); Publication No. US20040142478A1
(GENERAL IMFORMATION: Compositions and Methods Utilizing Sequences for Controlling Nucle
(TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for Controlling Nucle
(TITLE OF INVENTION: Acid Expression
(FILE REFERENCE: 3526.82543
(CURRENT APPLICATION NUMBER: US/10/776,213
(CURRENT APPLICATION NUMBER: US/10/776,213
(CURRENT FILING DATE: 2004-02-12
(NUMBER OF SEQ ID NOS: 32
(SOFTWARE: PatentIn Ver. 2.0
(SEQ ID NO 20
(LENGTH: 13073
(TYDE: DNA
(ORGANISM: Saccharomyces cerevisiae)
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                                                                                          tch 100.0%; Score 723; DB 18; al Similarity 100.0%; Pred. No. 2.7e-216; 723; Conservative 0; Mismatches 0;
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RESULT 4

US-10-776-213-30

US-10-776-213-30

Sequence 30, Application US/10776213

Publication No. US20040142478A1

GENERAL INFORMATION:
APPLICANT: ARITAZENECA AB

TITLE OF INVENTION: Compositions and Methods Utilizing Sequences for Controlling Nucl
TITLE OF INVENTION: Acid Expression
FILE REFERENCE: 3526.82543

CURRENT APPLICATION NUMBER: US/10/776,213

CURRENT FILING DATE: 2004-02-12

NUMBER OF SEQ ID NOS: 32

SOFTWARE: DATE: 2004-02-12

SOFTWARE: DATE: 2004-02-12

TYPE: DNA

ORGANISM: Saccharomyces Cerevisiae

US-10-776-213-30
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                                                 99.6%; Score 720.4; DB 18; 99.9%; Pred. No. 4e-216; tive 0; Mismatches 1;
                                                   Indels
                                                                                 Length
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                                                 0
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RESULT 5
US-10-451-467A-317
; Sequence 317, Application US/10451467A
; Publication No. US20040161840A1
; Publication No. US20040161840A1
; Publication No. US20040161840A1
; GENERAL INFORMATION;
APPLICANT: EBEEHARDT, INES
APPLICANT: LUTTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: LUTTEN, WALTER HERMAN MARIA LOUIS
APPLICANT: REEXWANS, RIEKA JOSEPHINA
TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
TITLE OF INVENTION: YEAST AND FUNGI
FILE REFERENCE: JAB-1667
; CURRENT FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: US/10/451,467A
; CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR APPLICATION NUMBER: EP 01870003.9
; PRIOR FILING DATE: 2001-01-04
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 732
; SOFTWARE: PatentIn version 3.1
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Sequence 198, Application US/10123155
Publication No. US20030068794A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desoryers, Luc
APPLICANT: Genoyers, Luc
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goodward, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
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US-10-123-155-198/c
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             APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C30
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Best Local
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ORGANISM: Saccharomyces
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498; Conservative
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NUMBER: US/10/123,155
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Pred. No. 7.7e-146;
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; Sequence 198, Application US/10146731
; Publication No. US20030129692A1
; GENERAL INFORMATION:
; APPLICANT: Baker; Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang

RESULT 7 US-10-146-731-198/c

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Prior Application remove
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 198
LENGTH: 1024
TYPE: PRT
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Best Local
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DM.S.M.ATMR...
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                          AAGACTAATAATAAC 721
                                                                     S.CWN.KTTR.DM.BT..H.M..SR.BM.RH.R...YMA
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C323
CURRENT APPLICATION NUMBER: US/10/146,731
CURRENT FILING DATE: 2002-05-15
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ORGANISM: Homo Sapien
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AAGACTAATAATAAC 721
                                 .YBBBCSMAAA.YRA.NG.TWT.RRASK..A.S.DHABWCH...BSA.B.KNS.S.RAT.
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NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
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TYPE: PRT
ORGANISM: Homo:
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CURRENT FILING DATE: 2002-05-06
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C168
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Gerritsen, Mary E.
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Wood, William
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US-10-141-761-198/c
; Sequence 198, Application US/10141761
; Publication No. US20030148432A1
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C198
CURRENT APPLICATION NUMBER: US/10/141,761
CURRENT APPLICATION NUMBER: US/10/141,761
CURRENT APPLICATION NUMBER: 002-05-08
Prior Application removed - See Palm or File Wrapper NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
TYDE: -THE TOTAL APPLICATION NOS: 550
LENGTH: 1024
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Best Local Similarity
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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US-10-142-885-198
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Query Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                                           SEQ ID NO 198
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C248
CURRENT APPLICATION NUMBER: US/10/142,885
CURRENT FILING DATE: 2002-05-10
                                                                                                                                                         Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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Watanabe, Colin K
Wood, William
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Filvaroff, Ellen
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DeForge, Laura
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      5.7%; Score 41; DB 16; Length 1024; 7.7%; Pred. No. 0.088; Indels 194; Mismatches 429; Indels
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APPLICANT: Beresini, Ma
APPLICANT: DeForge, Lau
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INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
INVENTION: ACIDS ENCODING THE SAME
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                                                                                                                       Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
                                               Watanabe, Colin K
Wood, William
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                   AND NUCLEIC
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LENGTH: 1024
TYPE: PRT
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Best Local
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CURRENT APPLICATION NUMBER: US/10/158,790
CURRENT FILING DATE: 2002-05-30
Prior Application removed - See File Wrap
NUMBER OF SEQ ID NOS: 550
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294
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52; Conserv
                                                                                                                          TTCMMRT.WH.BYH.HAT.B.SB.DSST.CH.KB.D.BHA.Y.M.KNWC.R.RH
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DM.S.M.ATMR...H
                            AAGACTAATAATAAC 721
                                                                                           GAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGG
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280
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RESULT 12
US-10-137-871-198/c
US-10-137-871-198/c
; Sequence 198, Application US/10137871
; Publication No. US20030207350A1
; GENERAL INFORMATION:
APPLICANT: Barker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura

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CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or Fi
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
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-10-137-871-198
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APPLICANT:
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YBBBCSMAAA, YRA.NG.TWT.RRASK..A.S.DHABWCH...BSA.B.KNS.S.RAT.
                                                            GAGTTGTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGACAGTTTCTGG
                                ACB...RDT.C.M.WBH.WWB.AB.HC.W.DG..DB.BKABH..RS.SSBS.H...Y..B
                                                                                                                                                                                        ..TTCMMRT.WH.BYH.HAT..B..SB.DSST.CH..KB.D.BHA..Y.M.KNWC.R.RH
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Stewar, Timothy A.

APPLICANT: Tumas, Daniel
APPLICANT: Wattanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Lang, Zemin
ITILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C188
CURRENT APPLICATION UNMBER: US/10/140,923
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION UNMBER: US/10/140,923
CURRENT FILING DATE: 2002-05-07
NUMBER OF SEQ ID NO 198
SEQ ID NO 198
LENGTH: 1024
TYPE: PPT
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; ORGANISM: Homo Sapien
US-10-140-923-198
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Best Local :
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APPLICANT: Baker, Kevin P.
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                                                                                       GAACAGGGGCTACAGTCTCGATAATAGAATAATAAGCGCATTTTTGCTAGCGCCGCCGCG
                                                                                                                      BS.B.DNY...H...YWNY.HRNBY.RCA.N.NC..WSCMH.RA.YDD.SMNSBW..T.S
                                                                                                                                                   GIGTATCTCACAGIGGTAACGGCACCGIGGCTCGGAAAACGGITCCTTCGIGACAATTCTA 346
                                                                                                                                                                                  RN.KYH..MH..R.TYSTTDW...HM..S.RY....N..RCTYT.S.THH..CTYNS
                                                                                                                                                                                                                  CCGTTGAAGCAACCGCACTATGACTAAAATGGTGCTGGACATCTCCATGGCTGTGACTTGT 286
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                             GCGCCCGTTTCCCAATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCCTATTTG
                                                             SBDSYNCBB
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                                                           A....W.RSNN..M.TMAMTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                5.7%; Score 41; DB 17; Length 1024; 7.7%; Pred. No. 0.088;
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                                                          3.HR..D.
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CURRENT APPLICATION NUMBER: US/10/141,756
CURRENT FILING DATE: 2002-05-08
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 198
LENGTH: 1024
TYPE: PRT
ORGANISM: Homo Sapien
US-10-141-756-198
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US-10-141-756-198/c
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Best Local S
Matches 52
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APPLICANT: Beresini, Maure
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Elle:
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     227
                                     834 ST..DGDMNC.SGT.K.B.YY...D.RST.B.SCN.NNM.WC.M.RAATB.M..R.N...N 775
                                                                                                             894 GA.T....MM.SBTAASD.MKW...WBH.H..SBCAGRB.HYBN...YNYNSS.WHS..A
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 CCGTTGAAGCAACCGCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGT 286
                                                                          CCGGGACCCCTCTCCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTATTCCTATC 226
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Godowski, Paul J.
Gurney, Austin L.
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                                                        ; ORGANISM: Homo US-10-141-759-198
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                                                                                           ; SEQ ID NO 198
; LENGTH: 1024
; TYPE: PRT
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Query Match
Best Local Similarity
                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/141,759
CURRENT FILING DATE: 2002-05-08
Prior Apploication removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C197
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Godowski, Paul J.
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Gerritsen, Mary E.
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Wood, William
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Filvaroff, Ellen
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                                                                          Sapien
5.7%; Score 41; DB 17; 7.7%; Pred. No. 0.088;
                 Length 1024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                          114 ...S.CWN.KTTR.DM.BT..H.M..SR.BM.RH.R....YMA.D.TRHCSCYY.TH.YTR
                                                                                                                                                                                                               474
                                                                                                                                                                                                                                                                             534 ..TTCMMRT.WH.BYH.HAT..B..SB.DSST.CH..KB.D.BHA..Y.M.KNWC.R.RH 475
                                                                                                                                                                                                                                                                                                                                                594 ..AW.HKB...NBRMCNYM.T.S.ANW.HNYTTNCRMD.A.RH..CY..BSDCK.NT.KY 535
                                                                                                                                                                                                                                                                                                                                                                                                              654 SBDSYNCBB.A....W.RSNN..M.TMAMTS.HR..D..A...YN.TAANC..A.B.RCK 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  714 BS.B.DNY...H...YWNY.HRNBY.RCA.N.NC..WSCMH.RA.YDD.SMNSBW..T.S 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   774 RN.KYH..MH..R.TYSTTDW...HM..S.RY.....N...RCTYT.S.THH..CTYNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       834 ST..DGDMNC.SGT.K.B.YY...D.RST.B.SCN.NNM.WC.M.RAATB.M..R.N..N
                                        707 AAGACTAATAATAAC 721
                                                                          354 YBBBCSMAAA.YRA.NG.TWT.RRASK..A.S.DHABWCH...BSA.B.KNS.S.RAT. 295
                                                                                                          587 GAGTTGTTTTTCAATCATATAAAAGGGAGAAATTGTTGCTCACTATGTGAÇAGTTTCTGG 646
                                                                                                                                                                                                                                             527 ATAAGGGATGTAACTTTCGATGAGAGAATTAGCAAGCGGAAAAAAACTATGGCTAGCTGG 586
                                                                                                                                                                                                                                                                                                                467 GGTAAGCCCCTTTCTGTTTTCGGCCAGTGGTTGCTGCAGGCTGCGCCGGAGAACATAGTG 526
                                                                                                                                                                                                                                                                                                                                                                                407 GCGCCCGTTTCCCAATAGGGAGGCGCAGTTTATCGGCGGAGCTCTACTTCTTTCCTATTTG 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 GAACAGGGGCTACAGTCTCGATAATAGAATAATAAGCGCATTTTTTGCTAGCGCCGCCGCG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 GTGTATCTCACAGTGGTAACGGCACCGTGGCTCGGAAACGGTTCCTTCGTGACAATTCTA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       227 CCGTTGAAGCAACCGCACTATGACTAAATGGTGCTGGACATCTCCATGGCTGTGACTTGT 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 CCGGGACCCCTCCTCCCCGCACGATTTCTTCCTTTCATATCTTCCTTTTATTCCTATC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          894 GA.T....MM.SBTAASD.MKW...WBH.H..SBCAGRB.HYBN...YNYNSS.WHS..A 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            954 T.CRYAN..MWMHY..MWT.HYCD.NYTBD..BH.TH.H.BB.SN.S.N..YN..NYHHS 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52; Conservative 194; Mismatches 429; Indels
DM.S.M.ATMR...H 280
                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       715
                                                                                                                                             355
                                                                                                                                                                                                             415
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Search completed: February 8, 2005, 00:37:03 Job time : 529 secs